Locus 333 (rs9901901)

SNiPAcard

Block annotations

Block info

genomic range	chr17:26,610,513-26,610,513
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	-0.216	gene(s) hit or close-by	KRT18P55
phastCons	0.996	eQTL gene(s)	SARM1, TMEM199, TMEM97
GERP++	-2.77	potentially regulated gene(s)	–
CADD score	1.06	disease gene(s)	–

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
SARM1	ENST00000585482	ILMN_1746265	adipocyte	1.70×10^{-6} (p-value)	MuTHER consortium	1
TMEM97	ENST00000226230	ILMN_1710962	blood	1.33×10^{-5} (p-value)	MuTHER consortium	1
TMEM97	ENST00000336687		adipocyte	4.53×10^{-7} (p-value)	MuTHER consortium	1
TMEM97	ENST00000582384					
TMEM199	ENST00000483505	ILMN_1748481	blood	2.43×10^{-5} (p-value)	Westra et al.	1
TMEM199	ENST00000509083					
TMEM199	ENST00000585027					
TMEM199	ENST00000292114					

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001535058 (promoter flanking region)	1	NHLF	DNase1
		embryonic stem cell (H1ESC)	DNase1
		HSMMtube	DNase1
		Osteobl	H3K27ac
		blood (DND-41)	H3K27me3
		skin (NHDF-AD)	DNase1
		breast (HMEC)	DNase1
		muscle (HSMM)	DNase1
		monocytes (Monocytes-CD14+)	H3K27me3
		lung (IMR90)	DNase1
		nervous (NH-A)	DNase1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
KRT18P55	ENST00000577198	?	?	1
KRT18P55	ENST00000578578	?	?	1

KRT18P55	ENST00000581956	?	?	1